

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Yoram Reiter
- (ii) TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-  
COMPATIBILITY COMPLEXES, CONSTRUCTS  
ENCODING SAME AND METHODS OF GENERATING  
SAME
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE:
- (B) STREET:
- (C) CITY:
- (D) STATE:
- (E) COUNTRY:
- (F) ZIP:
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
- (B) COMPUTER: Twinhead\* Slimnote-890TX
- (C) OPERATING SYSTEM: MS DOS version 6.2,  
Windows version 3.11
- (D) SOFTWARE: Word for Windows version 2.0 converted to  
an ASCII file
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME:
- (B) REGISTRATION NUMBER:
- (C) REFERENCE/DOCKET NUMBER:
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE:
- (B) TELEFAX:
- (C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:

10072000 00000000

(A) LENGTH: 9  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ile Met Asp Gln Val Pro Phe Ser Val

5

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Tyr Leu Glu Pro Gly Pro Val Thr Val

5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Leu Phe Gly Tyr Pro Val Tyr Val

5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1248  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGATCCAGC GTACTCCAAA GATTACGGTT TACTCACGTC ATCCAGCAGA 50  
 GAATGGAAAG TCAAATTTC TGAATTGCTA TGTGTCTGGG TTTCATCCAT 100  
 CCGACATTGA AGTTGACTTA CTGAAGAAAG GAGAGAGAAT TGAAAAAGTG 150  
 GAGCATTGAG ACTGTGCTTT CAGCAAGGAC TGGTCTTTCT ATCTCTTGTA 200  
 TTATACTGAG TTCACCCCCA CTGAAAAAGA TGAGTATGCC TGCCGTGTGA 250

ACCACGTGAC TTGTGCACAG CCCAAGATAG TTAAGTGGGA TCGAGACATG 300  
 GGTGGCGGTG GAAGCGCGGG TGGAGGCTCT GGTGGAGGTG GCAGCGGCTC 350  
 TCACTCCATG AGGTATTCTT TCACATPCGT GTCCCGGCCG GCGCGCGGG 400  
 AGCCCCGCTT CATCGCAGTG GGCTACGTGG ACGACACGCA GTTCGTGCGG 450  
 TTCGACAGCG ACGCCGCGAG CCAGAGGATG GAGCCGCGGG CGCCGTGGAT 500  
 AGAGCAGGAG GGTCCGGAGT ATTGGGACGG GGAGACACGG AAGCTGAGG 550  
 CCCACTCACA GACTCACCGA GTGGACCTGG GGAACCTGCG CGGCTACTAC 600  
 AACCAGAGCG AGGCCGGTTC TCACACCGTC CAGAGGATGT ATGGCTGCGA 650  
 CGTGGGGTCG GACTGGCGCT TCCTCCGCGG GTACCACGAG TACGCTAGC 700  
 ACGGCAAGGA TTACATCGCC CTGAAAGAGG ACCTGCGCTC TTGGACCGCG 750  
 GCGGACATGG CAGCTCAGAC CACCAAGCAC AAGTGGGAGG CGGCCCATGT 800  
 GCGCGAGCAG TTAGAGGCCT ACCTGGAGGG CACGTGCGTG GAGTGGCTCC 850  
 GCAGATACCT GGAGACGGG AAGGAGACGC TGCAGCGCAC GGACGCCCC 900  
 AAAACGCACA TGACTCACCA CGTGCTCTCT GACCATGAGG CCACCCCTGAG 950  
 GTGCTGGGCC CTGAGCTTCT ACCCTGCGGA GATCACACTG ACCTGGCAGC 1000  
 GGACTTGGAG GAATCTTTGA GGCANTGAAG ATGAGGCTGC GGGACTGA 1248

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro  
 5 10 15  
 Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly  
 20 25 30  
 Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu  
 35 40 45  
 Arg Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp  
 50 55 60  
 Trp Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu  
 65 70 75  
 Lys Asp Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln  
 80 85 90  
 Pro Lys Ile Val Lys Trp Asp Arg Asp Met Gly Gly Gly Gly Ser  
 95 100 105  
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser His Ser Met  
 110 115 120

Arg	Tyr	Phe	Phe	Thr	Ser	Val	Ser	Arg	Pro	Gly	Arg	Gly	Glu	Pro
				125					130					135
Arg	Phe	Ile	Ala	Val	Gly	Tyr	Val	Asp	Asp	Thr	Gln	Phe	Val	Arg
				140					145					150
Phe	Asp	Ser	Asp	Ala	Ala	Ser	Gln	Arg	Met	Glu	Pro	Arg	Ala	Pro
				155					160					165
Trp	Ile	Glu	Gln	Glu	Gly	Pro	Glu	Tyr	Trp	Asp	Gly	Glu	Thr	Arg
				170					175					180
Lys	Val	Lys	Ala	His	Ser	Gln	Thr	His	Arg	Val	Asp	Leu	Gly	Thr
				185					190					195
Leu	Arg	Gly	Tyr	Tyr	Asn	Gln	Ser	Glu	Ala	Gly	Ser	His	Thr	Val
				200					205					210
Gln	Arg	Met	Tyr	Gly	Cys	Asp	Val	Gly	Ser	Asp	Trp	Arg	Phe	Leu
				215					220					225
Arg	Gly	Tyr	His	Gln	Tyr	Ala	Tyr	Asp	Gly	Lys	Asp	Tyr	Ile	Ala
				230					235					240
Leu	Lys	Glu	Asp	Leu	Arg	Ser	Trp	Thr	Ala	Ala	Asp	Met	Ala	Ala
				245					250					255
Gln	Thr	Thr	Lys	His	Lys	Trp	Glu	Ala	Ala	His	Val	Ala	Glu	Gln
				260					265					270
Leu	Arg	Ala	Tyr	Leu	Glu	Gly	Thr	Cys	Val	Glu	Trp	Leu	Arg	Arg
				275					280					285
Tyr	Leu	Glu	Asn	Gly	Lys	Glu	Thr	Leu	Gln	Arg	Thr	Asp	Ala	Pro
				290					295					300
Lys	Thr	His	Met	Thr	His	His	Ala	Val	Ser	Asp	His	Glu	Ala	Thr
				305					310					315
Leu	Arg	Cys	Trp	Ala	Leu	Ser	Phe	Tyr	Pro	Ala	Glu	Ile	Thr	Leu
				320					325					330
Thr	Trp	Gln	Arg	Asp	Gly	Glu	Asp	Gln	Thr	Gln	Asp	Thr	Glu	Leu
				335					340					345
Val	Glu	Thr	Arg	Pro	Ala	Gly	Asp	Gly	Thr	Phe	Gln	Lys	Trp	Ala
				350					355					360
Ala	Val	Val	Val	Pro	Ser	Gly	Gln	Glu	Gln	Arg	Tyr	Thr	Cys	His
				365					370					375
Val	Gln	His	Glu	Gly	Leu	Pro	Lys	Pro	Leu	Thr	Leu	Arg	Trp	Glu
				380					385					390
Gln	Ser	Thr	Arg	Gly	Gly	Ala	Ser	Gly	Gly	Gly	Leu	Gly	Gly	Ile
				395					400					405
Phe	Glu	Ala	Met	Lys	Met	Glu	Leu	Arg	Asp					
				410					415					

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Ser His Ser Met Arg Tyr Phe Phe Thr Ser Val Ser Arg Pro  
 5 10 15  
 Gly Arg Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp  
 20 25 30  
 Thr Gln Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met  
 35 40 45  
 Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly Pro Glu Tyr Trp  
 50 55 60  
 Asp Gly Glu Thr Arg Lys Val Lys Ala His Ser Gln Thr His Arg  
 65 70 75  
 Val Asp Leu Gly Thr Leu Arg Gly Tyr Tyr Asn Gln Ser Glu Ala  
 80 85 90  
 Gly Ser His Thr Val Gln Arg Met Tyr Gly Cys Asp Val Gly Ser  
 95 100 105  
 Asp Trp Arg Phe Leu Arg Gly Tyr His Gln Tyr Ala Tyr Asp Gly  
 110 115 120  
 Lys Asp Tyr Ile Ala Leu Lys Glu Asp Leu Arg Ser Trp Thr Ala  
 125 130 135  
 Ala Asp Met Ala Ala Gln Thr Thr Lys His Lys Trp Glu Ala Ala  
 140 145 150  
 His Val Ala Glu Gln Leu Arg Ala Tyr Leu Glu Gly Thr Cys Val  
 155 160 165  
 Glu Trp Leu Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln  
 170 175 180  
 Arg Thr Asp Ala Pro Lys Thr His Met Thr His His Ala Val Ser  
 185 190 195  
 Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Ser Phe Tyr Pro  
 200 205 210  
 Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr  
 215 220 225  
 Gln Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr  
 230 235 240  
 Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Gln Glu Gln

10077300-024222

245	250	265
Arg Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu		
270	275	280
Thr Leu Arg Trp Glu Gln Ser Thr Arg Gly		
285	290	

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro		
5	10	15
Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly		
20	25	30
Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu		
35	40	45
Arg Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp		
50	55	60
Trp Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu		
65	70	75
Lys Asp Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln		
80	85	90
Pro Lys Ile Val Lys Trp Asp Arg Asp Met		
95	100	

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGGAGATATA CATATGGGCT CTCACCTCAT GAGGTA 36

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGCTTTGT TAGCACC GAT TCATAGTGA GGGGCTTGGG CAA 43

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
                   5                  10                  15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGAGATATAC ATATGATCCA GCGTACTCCA AAGAT 35

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGGGCTTTGT TAGCAGCCGA ATTCATTACA TGTCGATC CCACTTAAC 49

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAAGCGGTT GGCGCATATG ATCCAGCGTA CTCCAAAGAT T 41

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGAAGCGGCG GTGGAGGCTC TGTTGGAGGT GGCAGCGGCT CTCACTCCAT 50

GA

52

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAAGCGGCG GTGGAGGCTC TGTTGGAGGT GGCAGCGGCT CTCACTCCAT 50

GA

52

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGGAGAATTC TTACTCCCAT CTCAGGTGA GGGGCTTGGG CAA 43

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp

20250303 14:00:00



5

10

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gln Ser Thr Arg Gly Gly Ala Ser Gly Gly Gly

5

10

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAGTAAAGC TTTTATCAG CTCGGAAC CTGGATGCCT CCACGCCGAA 50  
 CTTCCACCAG AACCACTCC GGACCCGCCA CTCCTCTCC ATCTCAGGT 100

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGAATCTTTG AGGCAATGAA GATGGAGCTG CGGGACTGA 39

10072300 021003  
 000120 0022001